

Differential protein expression in Fe amended cultures of *Marinobacter aquaeolei*: a view into deep-sea metabolism.

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On early Earth, Fe was present in great quantities in its reduced ferrous form, readily available to the emerging biosynthetic pathways, possibly resulting in [the](#) high dependence on Fe in critical metabolic pathways. With the introduction of oxygen, through photosynthesis, this readily available pool of Fe was quickly lost through the abiotic oxidation to ferric Fe. However, the Fe requirements of many extant organisms do not reflect the scarcity of the element in the environments of today. In fact the diversity of modern bacteria that utilize ferrous iron as an electron donor is astounding, ranging from acidic to neutrophilic environments, from soils to the deepest trenches of the ocean and potentially even into the subsurface biosphere of the oceanic crust. Many of these deep ocean organisms oxidize Fe under anaerobic or microaerophilic conditions but the proteins involved are unknown.

Here we examine the production of Fe induced proteins in the deep-sea Fe-oxidizing *Marinobacter aquaeolei*. *M. aquaeolei* was grown under aerobic, chemoorganoheterotrophic conditions (5mM sodium citrate) with various concentrations of ferrous chloride (0, 200, 1300uM). Cells were harvested and the soluble proteins extracted. SDS-PAGE with Coomassie [brilliant blue](#) staining revealed the expression of protein bands [induced](#) in response to Fe addition. [Concurrent mutagenic studies \(A. Dhillon et al.\) suggest that Heme might be important in Fe-oxidation in M. aquaeolei.](#)

Therefore, we will attempt to assay and quantify Heme in these induced bands. ~~Proteins expressed in response to Fe additions will also be~~ These proteins were assayed for the presence of heme, as concurrent mutanogenic studies suggest heme may play a significant role in Fe oxidation for this organism.